AMENDMENTS TO THE CLAIMS WITH MARKINGS TO SHOW CHANGES MADE, AND LISTING OF ALL CLAIMS WITH PROPER IDENTIFIERS

1. (Previously presented) A method for determining a target nucleic acid sequence, the method comprising the steps of:

(a) contacting a preparation comprising a target nucleic acid sequence and a non-target nucleic acid sequence, the target nucleic acid sequence and the non-target nucleic acid sequence each having a first region of common sequence upstream of a first region of dissimilar sequence upstream of a second region of dissimilar sequence - with an oligonucleotide primer complementary to at least a portion of the first region of common sequence, under conditions to hybridize the primer thereto;

(b) contacting the resulting preparation with a first labeled nucleotide bearing a first label, wherein the first labeled nucleotide is complementary to a first template nucleotide comprised in the first region of dissimilar sequence of either the target nucleic acid sequence or the non-target nucleic acid sequence, under conditions to incorporate the first labeled nucleotide either into the primer hybridized to the target nucleic acid sequence or into the primer hybridized to the non-target nucleic acid sequence but not into both;

(c) subjecting the so treated preparation to a sequencing reaction, thereby extending the primer to form one or more first-labeled sequencing products comprising the first labeled nucleotide and one or more non-first-labeled sequencing products comprising no first labeled nucleotide; and

(d) determining the target nucleic acid sequence by determining at least a portion of the sequence of the first-labeled sequencing products and/or the non-first-labeled sequencing products, thereby determining at least the second region of dissimilar sequence of the target nucleic acid sequence.

2. (Previously presented) The method according to claim 1, wherein the target nucleic acid sequence and the non-target nucleic acid sequence each have a

second region of common sequence which lies between the first and second regions of dissimilar sequence.

3. (Previously presented) The method according to claim 1, wherein the method further comprises the step of separating the first-labelled sequencing products from the non-first-labeled sequencing products.

4. (Previously presented) The method according to claim 3, wherein the separating step comprises contacting the first-labeled and non-first-labeled sequencing products with a solid phase capable of binding to the first label.

5. (Previously presented) The method according to claim 4, wherein the solid phase comprises magnetic beads.

6. (Previously presented) The method according to claim 4, wherein the solid phase and the first label together comprise a ligand-affinant pair.

7. (Previously presented) The method according to claim 6, wherein the solid phase comprises streptavidin and the first label comprises biotin.

8. (Previously presented) The method according to claim 1, wherein the first label is fluorescent.

9. (Previously presented) The method according to claim 1, wherein the method comprises the further step of contacting the preparation of step (b) with a second labeled nucleotide bearing a second label before carrying out step (c), the second label being distinguishable from the first label, under conditions such that the non-first-labeled sequencing products but not the first-labeled sequencing products formed in step (c) include the second labeled nucleotide.

10. (Previously presented) The method according to claim 9, wherein the second label is fluorescent.

11. (Previously presented) The method according to claim 1, wherein the first labeled nucleotide is complementary to a first template nucleotide comprised in the first region of dissimilar sequence of the target nucleic acid sequence and the first labeled nucleotide is not complementary to a second template nucleotide at a corresponding position in the non-target nucleic acid sequence.

12. (Previously presented) The method according to claim 11, wherein the second labeled nucleotide is complementary to the second template nucleotide.

13. (Previously presented) A method for determining a target nucleic acid sequence and a second nucleic acid sequence as defined in claim 12, wherein step (d) comprises determining at least a portion of the sequence of the first-labeled sequencing products and the non-first-labeled sequencing products, thereby determining at least the second region of dissimilar sequence of each of the target nucleic acid sequence and the non-target nucleic acid sequence.

14. (Previously presented) The method according to claim 1, wherein the first region of dissimilar sequence comprises a single nucleotide.

15. (Previously presented) The method according to claim 1, wherein the second region of dissimilar sequence comprises a single nucleotide.

16. (Previously presented) The method according to claim 1, wherein the sequencing reaction comprises a method of sequencing based on the use of dideoxynucleotide terminators.

17. (Previously presented) The method according to claim 1, wherein the preparation comprises DNA derived from two or more subjects.

18. (Currently amended) A method for determining a plurality of target nucleic acid sequences, which method comprises the steps of:

(a) contacting a preparation wherein the plurality of target nucleic acid sequences is comprised in the preparation which further comprises a plurality of corresponding non-target nucleic acid sequences, each target nucleic acid sequence in the preparation corresponds to one or more corresponding non-target nucleic acid sequences in the preparation, each target nucleic acid sequence and each corresponding non-target nucleic acid sequence has a first region of common sequence upstream of a first region of dissimilar sequence upstream of a second region of dissimilar sequence, the first region of common sequence of each target nucleic acid sequence is the same as the first region of common sequence of its corresponding non-target nucleic acid sequences, the first region of dissimilar sequence of each target nucleic acid sequence is different to the first region of dissimilar sequence of its corresponding non-target nucleic acid sequences, the second region of dissimilar sequence of each target nucleic acid sequence is different to the second region of dissimilar sequence of its corresponding non-target nucleic acid sequences, - with a plurality of oligonucleotide primers, wherein each primer is complementary to at least a portion of the first region of common sequence of a target nucleic acid sequence and its corresponding non-target nucleic acid sequence, under conditions to hybridize the primer thereto; and

(b) contacting the resulting preparation with a plurality of first labeled nucleotides wherein each first labeled nucleotide bears a different first label, wherein each first labeled nucleotide is complementary to a first template nucleotide comprised in the first region of dissimilar sequence of a target nucleic acid under conditions to incorporate the first labeled nucleotide into the primer hybridized to the target nucleic acid sequence;

(c) subjecting the so treated preparation to a sequencing reaction, thereby extending each primer to form one or more first-labeled sequencing products comprising a first labeled nucleotide and one or more non-first-labeled sequencing products comprising no first labeled nucleotide; and

(d) determining at least a portion of the sequence of each different first-labeled sequencing product ~~and/or each non-first-labeled sequencing product~~, thereby determining at least the second region of dissimilar sequence of each target nucleic acid ~~sequence~~ sequences.

19. (Previously presented) The method according to claim 20, wherein the target nucleic acid sequence and the non-target nucleic acid sequence comprise one or more further regions of dissimilar sequence downstream of the second region of dissimilar sequence.

20. (Currently amended) A method for determining the haplotype of a subject from a sample comprising DNA from the subject according to the method as defined in claim 1, wherein the preparation comprises the sample, the target nucleic acid sequence comprises a locus on a first chromosome of a pair of chromosomes, the non-target ~~second~~ nucleic acid sequence comprises the corresponding locus on the second chromosome of the pair, the locus comprising two or more single nucleotide polymorphisms for which the subject is heterozygous, wherein the sequencing reaction is conducted to determine the sequence of the locus on the first and/or the second chromosome of the pair, thereby determining the haplotype of the subject.

21. (Previously presented) The method according to claim 20, wherein the locus comprises a human Class I or Class II HLA gene.

22. (Currently amended) A method of ~~pyrosequencing for~~ determining the haplotype of a subject comprising the steps of: ~~pyrosequencing is used on~~

- providing a sample comprising DNA from the subject to sequence a target locus on a first chromosome of a chromosome pair and a non-target locus on the second chromosome of the chromosome pair, wherein the target locus and the non-target locus each comprise ~~comprising~~ two or more single nucleotide polymorphisms, and wherein the subject is heterozygous at each single nucleotide polymorphism; providing a primer that hybridizes to the target locus and the non-target locus upstream of the first single nucleotide polymorphism;

- providing a first labeled nucleotide that is complementary to the nucleotide of the first single nucleotide polymorphism in either the target locus or the non-target locus wherein the label is a member of a ligand affinant pair;

- contacting the sample, the primer and the first labeled nucleotide under conditions to hybridize the primer to the target locus and the non-target locus and to incorporate the first labeled nucleotide into the primer hybridized to either the target locus or the non-target locus, but not both;

- separating the target locus/primer complex from the non-target locus/primer complex using the incorporated first labeled nucleotide;

- extending the primer of the target/locus primer complex and/or the non-target locus primer complex in a pyrophosphate sequencing reaction to thereby determining a haplotype of the subject ~~selecting a labeled nucleotide complementary to a nucleotide of the first single nucleotide polymorphism of one chromosome and labeling all sequencing products derived from one chromosome of a pair~~.

23.-25. (Canceled)